SCORE Search Results Details for Application 10573229 and Search Result 20090528_121105_us-10-573-229a-1.rnpbm.

This page gives you Search Results detail for the Application 10573229 and Search Result 20090528_121105_us-10-573-229a-1.rnpbm.

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GenCore version 6.3

OM nucleic - nucleic search, using sw model

Run on: May 31, 2009, 22:24:39 ; Search time 5012 Seconds
(without alignments)
5296.486 Million cell updates/sec

Title: US-10-573-229A-1
Perfect score: 920
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078765 seqs, 14427166270 residues

Total number of hits satisfying chosen parameters: 82157530

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_Main:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	1	920	100.0	920	19	US-10-573-229A-1	Sequence 1, Appli
	2	322.2	35.0	650	4	US-09-925-065A-602935	Sequence 602935,
	3	322.2	35.0	650	5	US-09-925-065A-602935	Sequence 602935,
	4	309.8	33.7	501	4	US-09-925-065A-602938	Sequence 602938,
	5	309.8	33.7	501	5	US-09-925-065A-602938	Sequence 602938,
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	7	149.8	16.3	872	28	US-11-443-428A-197866	Sequence 197866,
	8	149.6	16.3	485	4	US-09-925-065A-425353	Sequence 425353,
	9	149.6	16.3	485	5	US-09-925-065A-425353	Sequence 425353,
	10	122.6	13.3	561	3	US-09-854-867-108	Sequence 108, App
	11	122.6	13.3	561	11	US-10-786-970A-108	Sequence 108, App
	12	121.2	13.2	541	3	US-09-854-867-107	Sequence 107, App
	13	121.2	13.2	541	11	US-10-786-970A-107	Sequence 107, App
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c	19	109.6	11.9	590	4	US-09-925-065A-73588	Sequence 73588, A
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c	23	109.6	11.9	590	15	US-10-301-480-174827	Sequence 174827,
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	30	104.8	11.4	737	16	US-10-472-965-725	Sequence 725, App
	31	104.8	11.4	737	17	US-10-105-299-6677	Sequence 6677, Ap
	32	104.8	11.4	737	17	US-10-472-964-759	Sequence 759, App
	33	104.8	11.4	797	16	US-10-472-965-117	Sequence 117, App
	34	104.8	11.4	797	17	US-10-105-299-234	Sequence 234, App
	35	104.8	11.4	797	17	US-10-472-964-112	Sequence 112, App
	36	104.8	11.4	797	18	US-10-994-608-234	Sequence 234, App
	37	104.8	11.4	797	31	US-11-781-665-234	Sequence 234, App
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c	39	104.8	11.4	137000	13	US-10-515-538-11	Sequence 11, Appl
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ALIGNMENTS

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US-10-573-229A-1
; Sequence 1, Application US/10573229A
; Publication No. US20080166340A1
; GENERAL INFORMATION
;  APPLICANT: Ganymed Pharmaceuticals AG
;  APPLICANT:TURECI, Ozlem
;  APPLICANT:SAHIN, Ugur
;  APPLICANT:HELFTENBEIN, Gerd
;  APPLICANT:SCHLUTER, Volker
;  TITLE OF INVENTION: Identification of Tumour-Associated Cell Surface Antigens
;  TITLE OF INVENTION:for Diagnosis and Therapy
;  FILE REFERENCE: VOS-203
;  CURRENT APPLICATION NUMBER: US/10/573,229A
;  CURRENT FILING DATE: 2008-03-06
;  PRIOR APPLICATION NUMBER: PCT/EP2004/010697
;  PRIOR FILING DATE: 2004-09-23
;  PRIOR APPLICATION NUMBER: DE 103 44 799.7
;  PRIOR FILING DATE: 2003-09-26
;  NUMBER OF SEQ ID NOS: 312
;  SOFTWARE: PatentIn Version 3.1
; SEQ ID NO 1
;  LENGTH: 920
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-10-573-229A-1

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RESULT 2
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; Sequence 602935, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 602935
;   LENGTH: 650
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-602935

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Qy         733 CCGAACCCAAG 743
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RESULT 3
US-09-925-065A-602935
; Sequence 602935, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 602935
;   LENGTH: 650
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-602935

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  Best Local Similarity   95.4%;  Pred. No. 6.6e-93;
  Matches  354;  Conservative    0;  Mismatches   13;  Indels    4;  Gaps    2;

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RESULT 4
US-09-925-065A-602938
; Sequence 602938, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 602938
;   LENGTH: 501
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-602938

  Query Match   33.7%; Score 309.8; DB 4; Length 501;
  Best Local Similarity   94.5%; Pred. No. 6.3e-89;
  Matches 343; Conservative   0; Mismatches   17; Indels   3; Gaps   2;

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Db         61 GCTGTCCAGCTAAACCTCCAACCTCCAGATCCCATGCCAAGTTCTCTGCTTCTGCAAAAG 120

Qy        501 GACTTCAAGTGAAAGACATCTGCAGCTGTGAACGGGGGTAAAACCCTCCCTGCCCCAGGC 560
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Db        121 GACTTCAAGTGAAAGACATCTGCAGCTGTGAACGGGGGTAAAACCCTCCCTGCCCCAGGC 180

Qy        561 CCCAAGCAAGGATTTCCCTAGCGGGGAGGAAGGTAGAATCGAGAGACCTCTAACCCTGGG 620
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        181 CCCAAGCAAGGATTTCCCTAGCGGGGAGGAAGGTAGAATCGAAAGACCTCTAACCCTGGG 240

Qy        621 AGAGGAGGGAGGGAAATCTCCGAGGACCAGGGTTATGCAACAACACAAGGGAAGTACCTG 680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGAGGAGGGAGGGAAATCTCCGAGGACCAGGGTTATGCAACAACACAAGGGAAGTACCTG 300

Qy        681 CTGGGTTCTGGGGGTTGGGGAAGGAAAATCCCTACTGCCCCAAGAGCCAGCCCCGAACCC 740
              ||||  |   |||||  ||| ||||| |||||||||| |||||||||||| | ||  |
Db        301 CTGG--TTCTGGGGTCAGGGGAGGAAGATCCCTACTG-CCCAAGAGCCAGCACAGACACA 357

Qy        741 AAG 743
              | |
Db        358 AGG 360
```

RESULT 5
US-09-925-065A-602938
; Sequence 602938, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 602938
;   LENGTH: 501
;   TYPE: DNA
;   ORGANISM: Homo sapiens

US-09-925-065A-602938

Query Match 33.7%; Score 309.8; DB 5; Length 501;
Best Local Similarity 94.5%; Pred. No. 6.3e-89;
Matches 343; Conservative 0; Mismatches 17; Indels 3; Gaps 2;

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Qy        381 ACTGAGAAGCATCACCCACTTCCCCAGAACCTTTTTTACGTGGAGTGAAAACTTTAAGGG 440
              ||||||||||||||||||||||||||| |||||||||| ||||||||||||||||||||
Db          1 ACTGAGAAGCATCACCCACTTCCCCAGAGCCTTTTTTACATGGAGTGAAAACTTTAAGGG 60

Qy        441 GCTGTCCAGCTAAACCTCCAACCTCCAGATCCCATGCCAATTTCTCTGCTTCTGCAAAAG 500
              ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db         61 GCTGTCCAGCTAAACCTCCAACCTCCAGATCCCATGCCAAGTTCTCTGCTTCTGCAAAAG 120

Qy        501 GACTTCAAGTGAAAGACATCTGCAGCTGTGAACGGGGGTAAAACCCTCCCTGCCCCAGGC 560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACTTCAAGTGAAAGACATCTGCAGCTGTGAACGGGGGTAAAACCCTCCCTGCCCCAGGC 180

Qy        561 CCCAAGCAAGGATTTCCCTAGCGGGGAGGAAGGTAGAATCGAGAGACCTCTAACCCTGGG 620
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        181 CCCAAGCAAGGATTTCCCTAGCGGGGAGGAAGGTAGAATCGAAAGACCTCTAACCCTGGG 240

Qy        621 AGAGGAGGGAGGGAAATCTCCGAGGACCAGGGTTATGCAACAACACAAGGGAAGTACCTG 680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGAGGAGGGAGGGAAATCTCCGAGGACCAGGGTTATGCAACAACACAAGGGAAGTACCTG 300

Qy        681 CTGGGTTCTGGGGGTTGGGGAAGGAAAATCCCTACTGCCCCAAGAGCCAGCCCCGAACCC 740
              ||||  |   |||||  ||| ||||| |||||||||| |||||||||||| | ||  |
Db        301 CTGG--TTCTGGGGTCAGGGGAGGAAGATCCCTACTG-CCCAAGAGCCAGCACAGACACA 357

Qy        741 AAG 743
              | |
Db        358 AGG 360
```

RESULT 6
US-10-573-229A-267/c
; Sequence 267, Application US/10573229A
; Publication No. US20080166340A1
; GENERAL INFORMATION
; APPLICANT: Ganymed Pharmaceuticals AG
; APPLICANT:TURECI, Ozlem
; APPLICANT:SAHIN, Ugur
; APPLICANT:HELFTENBEIN, Gerd
; APPLICANT:SCHLUTER, Volker
; TITLE OF INVENTION: Identification of Tumour-Associated Cell Surface Antigens
; TITLE OF INVENTION:for Diagnosis and Therapy
; FILE REFERENCE: VOS-203
; CURRENT APPLICATION NUMBER: US/10/573,229A
; CURRENT FILING DATE: 2008-03-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/010697
; PRIOR FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: DE 103 44 799.7
; PRIOR FILING DATE: 2003-09-26
; NUMBER OF SEQ ID NOS: 312

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;  SOFTWARE: PatentIn Version 3.1
; SEQ ID NO 267
;  LENGTH: 390
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-10-573-229A-267

  Query Match             19.4%;  Score 178.2;  DB 19;  Length 390;
  Best Local Similarity   93.5%;  Pred. No. 2.7e-46;
  Matches  186;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy        328 ACCTCTGCTGTGGCCAATGCAGGAATGCTGGCCATCATTGCTTCTGCTGGGCGACTGAGA 387
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 ATCTCTGCTGTGGCCAATGCAGGAATGCTGGCCATCATTGCTTCTGCTGGGCGACTGAGA 205

Qy        388 AGCATCACCCACTTCCCCAGAACCTTTTTTACGTGGAGTGAAAACTTTAAGGGGCTGTCC 447
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 AGCATCACCCACTTCCCCAGAACCTTTTTTACGTGGAGTGAAAACTTTAAGGGGCTGTCC 145

Qy        448 AGCTAAACCTCCAACCTCCAGATCCCATGCCAATTTCTCTGCTTCTGCAAAAGGACTTCA 507
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 AGCTAAACCTCCAACCTCCAGATCCCATGCCAATTTCTCTGCTTCTGCAAAAGGACTCAT 85

Qy        508 AGTGAAAGACATCTGCAGC 526
                |  |  |  |||  ||||
Db         84 GGGCAGCGTTATCCACAGC 66


RESULT 7
US-11-443-428A-197866
; Sequence 197866, Application US/11443428A
; Publication No. US20070083334A1
; GENERAL INFORMATION:
;  APPLICANT: Mintz, Liat
;  APPLICANT:  Xie, Hanqing
;  APPLICANT:  Dahari, Dvir
;  APPLICANT:  Levanon, Erez
;  APPLICANT:  Freilich, Shiri
;  APPLICANT:  Beck, Nili
;  APPLICANT:  Zhu, Wei-Yong
;  APPLICANT:  Wasserman, Alon
;  APPLICANT:  Hermesh, Chen
;  APPLICANT:  Azar, Idit
;  APPLICANT:  Bernstein, Jeanne
;  TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
;  FILE REFERENCE: 02/23929
;  CURRENT APPLICATION NUMBER: US/11/443,428A
;  CURRENT FILING DATE:  2006-05-31
;  NUMBER OF SEQ ID NOS: 1034312
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 197866
;   LENGTH: 872
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-443-428A-197866
```

```
  Query Match             16.3%;  Score 149.8;  DB 28;  Length 872;
  Best Local Similarity   90.4%;  Pred. No. 5.9e-37;
  Matches  160;  Conservative    0;  Mismatches   17;  Indels    0;  Gaps    0;

Qy        127 ACTTTGGAAGCTGATCTTGGAGCACCAGTCAAGCCCTTAGCTGGCTGCAGCCACAGCCAA 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ACTTTGGAAGCTGATCTTGGAGCACCAGTCAAGCCCTTAGCTGGCTGCAGCCACAGCCAA 60

Qy        187 CAACAAGACTGCAACCTCCTGGGGGGATCCTGAGCCAGAATCCCCTGGCTAAATTGCTCCT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAACAAGACTGCAACCTCCTGGGGGGATCCTGAGCCAGAATCCCCTGGCTAAATTGCTCCT 120

Qy        247 TGATTCTTAACCCACAGAAATTGTGTAAGACCTCCATCAGGTGTCGACAAGGAAGAT 303
              |||||||||||||||||||||||    ||  |   |||  |  | |||||   ||
Db        121 TGATTCTTAACCCACAGAAATTGTGCTTAACACCATGCAGAAGCTGCCAAGGCTTAT 177


RESULT 8
US-09-925-065A-425353
; Sequence 425353, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 425353
;   LENGTH: 485
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-425353

  Query Match             16.3%;  Score 149.6;  DB 4;  Length 485;
  Best Local Similarity   91.0%;  Pred. No. 5.6e-37;
  Matches  193;  Conservative    0;  Mismatches   14;  Indels    5;  Gaps    3;

Qy        532 ACGGGGGTAAAACCCTCCCTGCCCCAGGCCCCAAGCAAGGATTTCCCTAGCGGGGAGGAA 591
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db          1 ACGGGGGTAAAACCTTCCCTGCCCCAGGCCCCAAGCAAGGATTTCCCTAGCGGGGAGGAA 60

Qy        592 GGTAGAATCGAGAGACCTCTAACCCTGGGAGAGGAGGGAGGGAAATCTCCGAGGACCAGG 651
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              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db          61 GGTAGAATCGAGAGACCTCTAA-CCTGGGAGAGGAGGGAGGGAAATCTCCGAGGACCAGG 119

Qy         652 GTTATGCAACAACACAAGGGAAGTACCTGCTGGGTTCTGGGGGTTGGGGAAGGAAAATCC 711
              |||||||||||||||||||||||||||||||    |  ||| | ||| ||||| ||||
Db         120 GTTATGCAACAACACAAGGGAAGTACCTGCTGG---TTCTGGGGTTGGGGAGGAAGATCC 176

Qy         712 CTACTGCCCCAAGAGCCAGCCCCGAACCCAAG 743
              |||||| |||||||||||| | ||  | | |
Db         177 CTACTG-CCCAAGAGCCAGCACAGACACAAGG 207


RESULT 9
US-09-925-065A-425353
; Sequence 425353, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 425353
;   LENGTH: 485
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-425353

  Query Match             16.3%;  Score 149.6;  DB 5;  Length 485;
  Best Local Similarity   91.0%;  Pred. No. 5.6e-37;
  Matches  193;  Conservative    0;  Mismatches   14;  Indels    5;  Gaps    3;

Qy         532 ACGGGGGTAAAACCCTCCCTGCCCCAGGCCCCAAGCAAGGATTTCCCTAGCGGGGAGGAA 591
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db           1 ACGGGGGTAAAACCTTCCCTGCCCCAGGCCCCAAGCAAGGATTTCCCTAGCGGGGAGGAA 60

Qy         592 GGTAGAATCGAGAGACCTCTAACCCTGGGAGAGGAGGGAGGGAAATCTCCGAGGACCAGG 651
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db          61 GGTAGAATCGAGAGACCTCTAA-CCTGGGAGAGGAGGGAGGGAAATCTCCGAGGACCAGG 119

Qy         652 GTTATGCAACAACACAAGGGAAGTACCTGCTGGGTTCTGGGGGTTGGGGAAGGAAAATCC 711
              |||||||||||||||||||||||||||||||    |  ||| | ||| ||||| ||||
Db         120 GTTATGCAACAACACAAGGGAAGTACCTGCTGG---TTCTGGGGTTGGGGAGGAAGATCC 176
```

```
Qy         712 CTACTGCCCCAAGAGCCAGCCCCGAACCCAAG 743
               |||||| |||||||||||||  ||   | | |
Db         177 CTACTG-CCCAAGAGCCAGCACAGACACAAGG 207
```

RESULT 10
US-09-854-867-108
; Sequence 108, Application US/09854867
; Publication No. US20030224356A1
; GENERAL INFORMATION:
; APPLICANT: JOAN, KNOLL H
; APPLICANT: ROGAN, PETER K
; TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING SAME
; FILE REFERENCE: 30307
; CURRENT APPLICATION NUMBER: US/09/854,867
; CURRENT FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 613
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 108
;   LENGTH: 561
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: repeat_region
;   LOCATION: (1)..(561)
;   OTHER INFORMATION: mlt1f1
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (62)..(62)
;   OTHER INFORMATION: n is a, c, g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (165)..(165)
;   OTHER INFORMATION: n is a, c, g or t
US-09-854-867-108

  Query Match   13.3%; Score 122.6; DB 3; Length 561;
  Best Local Similarity   69.6%; Pred. No. 3.3e-28;
  Matches 201; Conservative   0; Mismatches   74; Indels   14; Gaps   2;

```
Qy           2 CTGTAGAGGGGAATGGCTGCTGTGTCATGGGGGTGCATGAGCAGCCCAGTGGAGAGGTGC 61
               || | | ||      |||||  ||||||| ||   |   |||||||| |||||||||  |
Db         201 CTCTGGGGGAAGCCAGCTGCCATGTCATGAGGACACTCAAGCAGCCCTGTGGAGAGGCCC 260

Qy          62 ACTTGGTGAGAAACCGATGCCT-CTGCCAACCACCTGCACTAACCTGCTGGGTC------ 114
               |  |||  || ||| || |||| ||||||||  || |||   | |||  |  ||
Db         261 ATGTGGCAAGGAACTGAGGCCTCCTGCCAACAGCCAGCAAGGAACTGAGGCCTCCTGCCA 320

Qy         115 -------TGAGACTGAGCCACTTTGGAAGCTGATCTTGGAGCACCAGTCAAGCCCTTAGC 167
                     || || |||||||  |||||||| |||| |  ||| |||||||||| | ||
Db         321 ACAGCCATGTGAGTGAGCCATCTTGGAAGCAGATCCTCCAGCCCCAGTCAAGCCTTCAGA 380

Qy         168 TGGCTGCAGCCACAGCCAACAACAAGACTGCAACCTCCTGGGGGATCCTGAGCCAGAATC 227
```

```
              || |||||||| |||| |||| |  |||||||||||| || | || |||||||||||| |
Db         381 TGACTGCAGCCCCAGCTAACATCTTGACTGCAACCTCATGAGAGACCCTGAGCCAGAACC 440

Qy         228 CCCTGGCTAAATTGCTCCTTGATTCTTAACCCACAGAAATTGTGTAAGA 276
                ||  |||||  |||||||  |||| | |||||||||||| ||||  |||
Db         441 ACCCAGCTAAGCTGCTCCTAAATTCCTGACCCACAGAAACTGTGAGAGA 489
```

RESULT 11
US-10-786-970A-108
; Sequence 108, Application US/10786970A
; Publication No. US20050064449A1
; GENERAL INFORMATION:
; APPLICANT: JOAN, KNOLL
; APPLICANT: ROGAN, PETER
; TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING SAME
; FILE REFERENCE: 30307
; CURRENT APPLICATION NUMBER: US/10/786,970A
; CURRENT FILING DATE: 2004-02-24
; PRIOR APPLICATION NUMBER: US/09/573,080
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 479
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 108
;   LENGTH: 561
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: repeat_region
;   LOCATION: (1)..(561)
;   OTHER INFORMATION: mlt1f1
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: n is a, c, g or t
; PUBLICATION INFORMATION:
; PUBLICATION INFORMATION:
;   AUTHORS: Jurka, J; Walichiewicz, J; Milosavljevic, A
;   TITLE: Prototypic sequences for human repetitive DNA
;   JOURNAL: Journal of Molecular Evolution
;   VOLUME: 35
;   ISSUE: 4
;   PAGES: 286-291
;   DATE: 1992-10-__
;   DATABASE ACCESSION NUMBER: Database of repetitive elements (repbase)
;   DATABASE ENTRY DATE: _____-__-__
;   DATABASE ENTRY DATE: 1996-01-26
US-10-786-970A-108

  Query Match   13.3%; Score 122.6; DB 11; Length 561;
  Best Local Similarity   69.6%; Pred. No. 3.3e-28;
  Matches 201; Conservative   0; Mismatches   74; Indels   14; Gaps   2;

```
Qy           2 CTGTAGAGGGGAATGGCTGCTGTGTCATGGGGGTGCATGAGCAGCCCAGTGGAGAGGTGC 61
               || | | ||      |||||  ||||||| ||   |   |||||||| |||||||||  |
Db         201 CTCTGGGGGAAGCCAGCTGCCATGTCATGAGGACACTCAAGCAGCCCTGTGGAGAGGCCC 260
```

```
Qy          62 ACTTGGTGAGAAACCGATGCCT-CTGCCAACCACCTGCACTAACCTGCTGGGTC------ 114
               |  |||  || ||| || |||| ||||||||  || |||   | |||  |  ||
Db         261 ATGTGGCAAGGAACTGAGGCCTCCTGCCAACAGCCAGCAAGGAACTGAGGCCTCCTGCCA 320

Qy         115 -------TGAGACTGAGCCACTTTGGAAGCTGATCTTGGAGCACCAGTCAAGCCCTTAGC 167
                     || || |||||||  |||||||| |||| |  ||| |||||||||||| | ||
Db         321 ACAGCCATGTGAGTGAGCCATCTTGGAAGCAGATCCTCCAGCCCCAGTCAAGCCTTCAGA 380

Qy         168 TGGCTGCAGCCACAGCCAACAACAAGACTGCAACCTCCTGGGGGGATCCTGAGCCAGAATC 227
               || |||||||| |||| |||| |  |||||||||||| || | || |||||||||||| |
Db         381 TGACTGCAGCCCCAGCTAACATCTTGACTGCAACCTCATGAGAGACCCTGAGCCAGAACC 440

Qy         228 CCCTGGCTAAATTGCTCCTTGATTCTTAACCCACAGAAATTGTGTAAGA 276
                ||  |||||  |||||||  |||| | |||||||||||| ||||  |||
Db         441 ACCCAGCTAAGCTGCTCCTAAATTCCTGACCCACAGAAACTGTGAGAGA 489
```

RESULT 12
US-09-854-867-107
; Sequence 107, Application US/09854867
; Publication No. US20030224356A1
; GENERAL INFORMATION:
; APPLICANT: JOAN, KNOLL H
; APPLICANT: ROGAN, PETER K
; TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING SAME
; FILE REFERENCE: 30307
; CURRENT APPLICATION NUMBER: US/09/854,867
; CURRENT FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 613
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 107
;   LENGTH: 541
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: repeat_region
;   LOCATION: (1)..(541)
;   OTHER INFORMATION: mlt1f
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (179)..(179)
;   OTHER INFORMATION: n is a, c, g or t
US-09-854-867-107

  Query Match   13.2%; Score 121.2; DB 3; Length 541;
  Best Local Similarity   68.8%; Pred. No. 9.4e-28;
  Matches 190; Conservative   3; Mismatches   81; Indels   2; Gaps   2;

```
Qy           2 CTGTAGAGGGGAATGGCTGCTGTGTCATGGGGGTGCATGAGCAGCCCAGTGGAGAGGTGC 61
               || | | ||      |||||  ||  |||  |   |   ||||||| | |||||| || |
Db         197 CTCTGGGGGAAGCCAGCTGCCATGCTATGAAGACACTCAAGCAGCCTA-TGGAGAAGTCC 255

Qy          62 ACTTGGTGAGAAACCGATGCCT-CTGCCAACCACCTGCACTAACCTGCTGGGTCTGAGAC 120
```

```
              || |||  || ||| || | || ||||||||  || ||    ||:|||  |   || ||
Db         256 ACGTGGSAAGGAACTGAGGTCTCCTGCCAACAGCCAGCTTCGACYTGCCAGCCATGTGAG 315

Qy         121 TGAGCCACTTTGGAAGCTGATCTTGGAGCACCAGTCAAGCCCTTAGCTGGCTGCAGCCAC 180
              |||||||  |||||||| |||| |  ||| |||||:||||| | || || |||||||| |
Db         316 TGAGCCATCTTGGAAGCGGATCCTCCAGCCCCAGTYAAGCCTTCAGATGACTGCAGCCCC 375

Qy         181 AGCCAACAACAAGACTGCAACCTCCTGGGGGGATCCTGAGCCAGAATCCCCTGGCTAAATT 240
               ||  ||| |  |||||||||||| || | || ||||||||||||   ||  |||||  |
Db         376 GGCTGACATCTTGACTGCAACCTCATGAGAGACCCTGAGCCAGAACTACCCAGCTAAGCT 435

Qy         241 GCTCCTTGATTCTTAACCCACAGAAATTGTGTAAGA 276
              |||||| :|||| | |||||||||||| ||||  | |
Db         436 GCTCCTARATTCCTGACCCACAGAAACTGTGAGATA 471


RESULT 13
US-10-786-970A-107
; Sequence 107, Application US/10786970A
; Publication No. US20050064449A1
; GENERAL INFORMATION:
;  APPLICANT: JOAN, KNOLL
;  APPLICANT:  ROGAN, PETER
;  TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING
SAME
;  FILE REFERENCE: 30307
;  CURRENT APPLICATION NUMBER: US/10/786,970A
;  CURRENT FILING DATE:  2004-02-24
;  PRIOR APPLICATION NUMBER: US/09/573,080
;  PRIOR FILING DATE: 2000-05-16
;  NUMBER OF SEQ ID NOS: 479
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 107
;   LENGTH: 541
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: repeat_region
;   LOCATION: (1)..(541)
;   OTHER INFORMATION: mlt1f
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: n is a, c, g or t
;  PUBLICATION INFORMATION:
;  PUBLICATION INFORMATION:
;   AUTHORS: Jurka, J; Walichiewicz, J; Milosavljevic, A
;   TITLE: Prototypic sequences for human repetitive DNA
;   JOURNAL: Journal of Molecular Evolution
;   VOLUME: 35
;   ISSUE: 4
;   PAGES: 286-291
;   DATE: 1992-10-__
;   DATABASE ACCESSION NUMBER: Database of repetitive elements (repbase)
;   DATABASE ENTRY DATE: _____-__-__
;   DATABASE ENTRY DATE: 1996-01-26
US-10-786-970A-107
```

```
  Query Match             13.2%;  Score 121.2;  DB 11;  Length 541;
  Best Local Similarity   68.8%;  Pred. No. 9.4e-28;
  Matches  190;  Conservative    3;  Mismatches   81;  Indels    2;  Gaps    2;

Qy          2 CTGTAGAGGGGAATGGCTGCTGTGTCATGGGGGTGCATGAGCAGCCCAGTGGAGAGGTGC 61
              || | | ||      |||||  ||  |||  |   |   ||||||| | |||||| || |
Db        197 CTCTGGGGGAAGCCAGCTGCCATGCTATGAAGACACTCAAGCAGCCTA-TGGAGAAGTCC 255

Qy         62 ACTTGGTGAGAAACCGATGCCT-CTGCCAACCACCTGCACTAACCTGCTGGGTCTGAGAC 120
              || |||  || ||| || | || ||||||||  || ||    ||:|||  |   || ||
Db        256 ACGTGGSAAGGAACTGAGGTCTCCTGCCAACAGCCAGCTTCGACYTGCCAGCCATGTGAG 315

Qy        121 TGAGCCACTTTGGAAGCTGATCTTGGAGCACCAGTCAAGCCCTTAGCTGGCTGCAGCCAC 180
              |||||||  |||||||| |||| |  ||| |||||:||||| | || || |||||||| |
Db        316 TGAGCCATCTTGGAAGCGGATCCTCCAGCCCCAGTYAAGCCTTCAGATGACTGCAGCCCC 375

Qy        181 AGCCAACAACAAGACTGCAACCTCCTGGGGGATCCTGAGCCAGAATCCCCTGGCTAAATT 240
               ||  ||| |  |||||||||||| || | || ||||||||||||   ||  |||||  |
Db        376 GGCTGACATCTTGACTGCAACCTCATGAGAGACCCTGAGCCAGAACTACCCAGCTAAGCT 435

Qy        241 GCTCCTTGATTCTTAACCCACAGAAATTGTGTAAGA 276
              |||||| :|||| | |||||||||||| ||||  | |
Db        436 GCTCCTARATTCCTGACCCACAGAAACTGTGAGATA 471


RESULT 14
US-09-925-065A-176178/c
; Sequence 176178, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 176178
;   LENGTH: 493
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-176178
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  Query Match             13.0%;  Score 119.6;  DB 4;  Length 493;
  Best Local Similarity   66.7%;  Pred. No. 3e-27;
  Matches  184;  Conservative    1;  Mismatches   90;  Indels    1;  Gaps    1;

Qy          2 CTGTAGAGGGGAATGGCTGCTGTGTCATGGGGGTGCATGAGCAGCCCAGTGGAGAGGTGC 61
              || | ||||      ||||||||||||||| |||  |   | ||||||  || |||||| |
Db        419 CTCTGGAGGAAGTCAGCTGCTGTGTCATGAGGGCACTCAAACAGCCCTATGAAGAGGTCC 360

Qy         62 ACTTGGTGAGAAACCGATGCC-TCTGCCAACCACCTGCACTAACCTGCTGGGTCTGAGAC 120
              |  |||| || ||| || | | |||||||||  || ||| |||| |||  ||| || ||
Db        359 ATGTGGTAAGGAACTGAGGACTTCTGCCAACAGCCAGCAATAACTTGCCAGGTATGTGAA 300

Qy        121 TGAGCCACTTTGGAAGCTGATCTTGGAGCACCAGTCAAGCCCTTAGCTGGCTGCAGCCAC 180
              || ||||  ||||||||   |  |  | | |||| ||||| ||    |  |||  ||| |
Db        299 TGTGCCATCTTGGAAGCAAGTTCTCCAACTCCAGACAAGCTCTCTAATAACTGTGGCCCC 240

Qy        181 AGCCAACAACAAGACTGCAACCTCCTGGGGGGATCCTGAGCCAGAATCCCCTGGCTAAATT 240
              |||  ||| |  | |||||||| |  | ||||  ||||||||| | | ||  |:|||
Db        239 AGCTGACATCTTGGCTGCAACCCCACGAGGGAATCTGAGCCAGCACCACCAAGMTAAGCC 180

Qy        241 GCTCCTTGATTCTTAACCCACAGAAATTGTGTAAGA 276
               |||||  |||| | ||   |||||| ||||| | |
Db        179 ACTCCTAAATTCCTGACTTGCAGAAAATGTGTGAAA 144


RESULT 15
US-09-925-065A-176178/c
; Sequence 176178, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 176178
;   LENGTH: 493
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-176178

  Query Match             13.0%;  Score 119.6;  DB 5;  Length 493;
  Best Local Similarity   66.7%;  Pred. No. 3e-27;
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  Matches  184;  Conservative    1;  Mismatches   90;  Indels    1;  Gaps    1;

Qy          2 CTGTAGAGGGGAATGGCTGCTGTGTCATGGGGGTGCATGAGCAGCCCAGTGGAGAGGTGC 61
              || | ||||      |||||||||||||| |||  |   | ||||||  || |||||| |
Db        419 CTCTGGAGGAAGTCAGCTGCTGTGTCATGAGGGCACTCAAACAGCCCTATGAAGAGGTCC 360

Qy         62 ACTTGGTGAGAAACCGATGCC-TCTGCCAACCACCTGCACTAACCTGCTGGGTCTGAGAC 120
              |  |||| || ||| || | | |||||||||  || ||| |||| |||  ||| || ||
Db        359 ATGTGGTAAGGAACTGAGGACTTCTGCCAACAGCCAGCAATAACTTGCCAGGTATGTGAA 300

Qy        121 TGAGCCACTTTGGAAGCTGATCTTGGAGCACCAGTCAAGCCCTTAGCTGGCTGCAGCCAC 180
              || ||||  |||||||   |  |  | | |||| ||||| ||    |  |||  ||| |
Db        299 TGTGCCATCTTGGAAGCAAGTTCTCCAACTCCAGACAAGCTCTCTAATAACTGTGGCCCC 240

Qy        181 AGCCAACAACAAGACTGCAACCTCCTGGGGGGATCCTGAGCCAGAATCCCCTGGCTAAATT 240
              |||  ||| |  | |||||||| |  | ||||  ||||||||| | | ||  |:|||
Db        239 AGCTGACATCTTGGCTGCAACCCCACGAGGGAATCTGAGCCAGCACCACCAAGMTAAGCC 180

Qy        241 GCTCCTTGATTCTTAACCCACAGAAATTGTGTAAGA 276
               |||||  |||| | ||   |||||| ||||| | |
Db        179 ACTCCTAAATTCCTGACTTGCAGAAAATGTGTGAAA 144


Search completed: May 31, 2009, 23:48:17
Job time : 5018 secs
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